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promoter is characterized by its retention of at least 20, 30, 40, 50, or 60 consecutive nucleic acid residues of the disclosed promoter sequences (SEQ ID NOS: 17, 22, 23, 24, and 25).

Please amend the claims as follows. For the Examiner's convenience, claims that have not been amended are denoted as "reiterated."

a2 Sub B1  
~~1. (Amended) A recombinant promoter, capable of driving expression of a transgene operably linked to the promoter, wherein the promoter comprises a nucleic acid sequence that shares at least 80% sequence identity to SEQ ID NO: 25.~~

Please cancel claims 2-6.

7. (Amended) A vector, comprising the recombinant promoter of claim 1.

8. (Amended) A host cell, comprising the vector of claim 7.

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9. (Amended) A transgenic plant, comprising the host cell of claim 8.

10. (Amended) A transgene, comprising the promoter of claim 1 and at least one ORF operably linked to the promoter.

11. (Amended) A vector, comprising the transgene of claim 10.

12. (Amended) A plant cell, comprising the transgene of claim 10.

13. (Reiterated) The transgene of claim 10, wherein the ORF encodes a cationic peptide.

a4 Sub B2  
~~14. (Amended) The plant cell of claim 12, wherein the plant cell is obtained from a plant selected from the group consisting of maize, wheat, rice, millet, tobacco, sorghum, rye, barley, brassica, sunflower, seaweeds, lemma, oat, soybean, cotton, legumes, rape/canola, alfalfa, flax, sunflower, safflower, brassica, cotton, flax, peanut, and clover; lettuce, tomato, cucurbits,~~

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cassava, potato, carrot, radish, pea, lentil, cabbage, cauliflower, broccoli, Brussel sprouts, peppers, other vegetables, citrus, apples, pears, peaches, apricots, walnuts, other fruit trees, orchids, carnations, roses, other flowers, cacao; poplar, elms, other deciduous trees, pine, Douglas-fir, spruce, other conifers, turf grasses, cacao, rubber trees and members of the genus *Hevea*.

15. (Amended) A method for expressing at least one protein in a host cell, comprising:  
introducing a transgene comprising an ORF and the recombinant promoter of claim 1 into a host cell; and  
allowing the host cell to produce a protein from the ORF.

16. (Amended) The method of claim 15, wherein the host cell is a plant host cell.

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17. (Reiterated) A protein, expressed according to the method of claim 15.

18. (Reiterated) The protein of claim 17, wherein the protein is a cationic peptide.

19. (Reiterated) The recombinant promoter of claim 1, wherein the promoter is developmental-specific.

20. (Reiterated) The promoter of claim 1, wherein the promoter is induced with ethylene or a metal.

21. (Reiterated) The recombinant promoter of claim 19, wherein the promoter is expressable in gametophytic tissue.

22. (Reiterated) A recombinant promoter, comprising at least eight promoter elements selected from the group consisting of E-box motifs (SEQ ID NO: 1), ERE elements (SEQ ID NO: 20), AT-rich regions (SEQ ID NO: 3), MRE elements (SEQ ID NO: 21), ACGT core elements (SEQ ID NO: 4), and duplicates thereof, wherein the promoter displays promoter activity.

23. (Reiterated) The recombinant promoter of claim 22, wherein the promoter comprises at least ten promoter elements.

24. (Reiterated) The recombinant promoter of claim 22, comprising the following promoter elements: 3'-ERE element (SEQ ID NO: 20), AT-rich region (SEQ ID NO: 3), ERE element (SEQ ID NO: 20), ERE element (SEQ ID NO: 20), E-box motif (SEQ ID NO: 1), MRE element (SEQ ID NO: 21), ACGT core element (SEQ ID NO: 4), ACGT core element (SEQ ID NO: 4), and ACGT core element (SEQ ID NO: 4)-5'.

25. (Reiterated) A vector, comprising the promoter of claim 22 operably linked to an ORF.

26. (Amended) A host cell, comprising the vector of claim 25.

27. (Amended) A transgenic plant, comprising the vector of claim 25.

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28. (Amended) The transgenic plant of claim 27, wherein the transgenic plant is selected from the group consisting of maize, wheat, rice, millet, tobacco, sorghum, rye, barley, brassica, sunflower, seaweeds, lemna, oat, soybean, cotton, legumes, rape/canola, alfalfa, flax, sunflower, safflower, brassica, cotton, flax, peanut, and clover; lettuce, tomato, cucurbits, cassava, potato, carrot, radish, pea, lentil, cabbage, cauliflower, broccoli, Brussel sprouts, peppers, other vegetables, citrus, apples, pears, peaches, apricots, walnuts, other fruit trees, orchids, carnations, roses, other flowers, cacao; poplar, elms, other deciduous trees, pine, Douglas-fir, spruce, other conifers, turf grasses, cacao, rubber trees and members of the genus *Hevea*.

29. (Reiterated) The vector of claim 25, wherein the ORF encodes a cationic peptide.

Please add the following claims:

30. (New) The plant cell of claim 14, wherein the plant cell is obtained from a tobacco plant.

31. (New) The plant cell of claim 14, wherein the plant cell is obtained from a potato plant.

32. (New) The plant cell of claim 14, wherein the plant cell is obtained from a wheat plant.

26 33. (New) The plant cell of claim 14, wherein the plant cell is obtained from a Douglas-fir plant.

Sub 33 34. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 25.

35. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 25.

36. (New) The promoter of claim 1, wherein the promoter comprises at least 20 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 25.

37. (New) The promoter of claim 1, wherein the promoter comprises at least 20 consecutive nucleic acid residues of the nucleic acid sequence shown in SEQ ID NO: 25.

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39. (New) The promoter of claim 1, wherein the promoter comprises at least 40 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 25.

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40. (New) The promoter of claim 1, wherein the promoter comprises at least 40 consecutive nucleic acid residues of the nucleic acid sequence shown in SEQ ID NO: 25.

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41. (New) The promoter of claim 1, wherein the promoter comprises at least 60 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 25.

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42. (New) The promoter of claim 1, wherein the promoter comprises at least 60 consecutive nucleic acid residues of the nucleic acid sequence shown in SEQ ID NO: 25.

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43. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 24.

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44. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 24.

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45. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 24.

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46. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 23.

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47. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 23.

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48. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 23.

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49. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 22.